

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

OCR-754.CIP

Applicants	James M. Anderson and Christina M. Van Itallie
Serial No. - pending	Filing Date: June 25, 2001
Art Unit 1644	Examiner Patrick Nolan
Title of Application	Human Occludin, Its Uses and Enhancement of Drug Absorption Using Occludin Inhibitors

Commissioner of Patents
and Trademarks
Washington, DC 20231

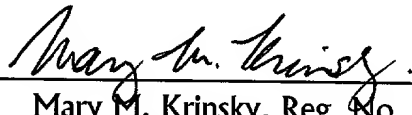
SUBMISSION OF A SEQUENCE STATEMENT UNDER 37 C.F.R. § 1.821(g)

Dear Sir:

The computer-readable form submitted herewith with an application that is a C.I.P. of U.S. application serial number 09/142,732, filed September 15, 1998, is identical to the Sequence Listing of its parent case and that filed in the international parent case, PCT/US97/05809, filed March 14, 1997, and contains no new matter.

Respectfully submitted,

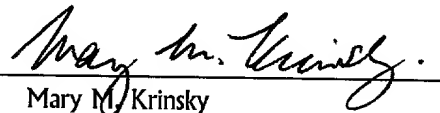
June 25, 2001 by



Mary M. Krinsky, Reg. No. 32423
79 Trumbull Street
New Haven, CT 06511-3708
(203) 773-9544

I hereby certify that this paper and the application are today being deposited with the United States Postal Service as Express Mail, no. EL572277375US, under 37 C.F.R. § 1.10 in an envelope addressed to the Box New Application, Commissioner of Patents, Washington, D.C. 20231.

June 25, 2001



Mary M. Krinsky

1/7
SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANTS: James M. Anderson
Christina M. Van Itallie
- (ii) TITLE OF INVENTION: Human Occludin, Its Uses
and Enhancement of Drug Absorption Using Occlu-
din Inhibitors
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSEE: Yale University Medical School
Section of Pulmonary and Critical Care Medicine
Department of Internal Medicine
 - (B) STREET: 333 Cedar Street, LCI 105
 - (C) CITY: New Haven
 - (D) STATE: Connecticut
 - (E) COUNTRY: United States of America
 - (F) ZIP CODE: 065220-8057
- (v) COMPUTER READABLE FORM
 - (A) MEDIUM TYPE: 3.5" 1.44 Mb diskette
 - (B) COMPUTER: IBM PC
 - (C) OPERATING SYSTEM: MS DOS
 - (D) SOFTWARE: Word Processing
- (vi) CURRENT APPLICATION DATA
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: June 25, 2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
 - (A) APPLICATION NUMBER: U.S. 09/142,732
 - (B) FILING DATE: September 15, 1998
 - (C) CLASSIFICATION: 530-350.000
- (viii) ATTORNEY INFORMATION
 - (A) NAME: Mary M. Krinsky
 - (B) REGISTRATION NO.: 32423
 - (C) REFERENCE/DOCKET NUMBER: OCR-754.CIP
- (ix) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE NUMBER: 203-773-9544
 - (B) TELEFAX NUMBER: 203-773-1183

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2312
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: cDNA

(v) FRAGMENT TYPE: complete sequence

(ix) FEATURE:

- (A) NAME/KEY: human occludin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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GCCTCTCTCC ATCAGACACC CCAAGGTTCC ATCCGAAGCA GCGGAGCAC   50
CGAACGCACC CCGGGGTGGT CAGGGACCCC CATCCGTGCT GCCCCCTAGG  100
AGCCCGCGCC TCTCCTCTGC GCCCCGCCTC TCGGGCCGCA ACATCGCGCG  150
GTTCTTTTAA CAGCGCGCTG GCAGGGTGTG GGAAGCAGGA CCGCGTCCTC  200
CCGCCCCCTC CCATCCGAGT TTCAGGTGAA TTGGTCACCG AGGGAGGAGG  250
CCGACACACC ACACCTACAC TCCCGCGTCC ACCTCTCCCT CCCTGCTTCC  300
TCTTGGCGGA GGCGGCAGGA ACCGAGAGCC AGGTCCAGAG CGCCGAGGAG  350
CCGGTCTAGG ACGCAGCAGA TTGGTTTATC TTGGAAGCTA AAGGGCATTG  400
CTCATCCTGA AGATCAGCTG ACCATTGACA ATCAGCCATG TCATCCAGGC  450
CTCTTGAAAG TCCACCTCCT TACAGGCCTG ATGAATTCAA ACCGAATCAT  500
TATGCACCAA GCAATGACAT ATATGGTGGA GAGATGCATG TTCGACCAAT  550
GCTCTCTCAG CCAGCCTACT CTTTTTACCC AGAAGATGAA ATTCTTCACT  600
TCTACAAATG GACCTCTCCT CCAGGAGTGA TTCGGATCCT GTCTATGCTC  650
ATTATTGTGA TGTGCATTGC CATCTTTGCC TGTGTGGCCT CCACGCTTGC  700
CTGGGACAGA GGCTATGGAA CTTCCCTTTT AGGAGGTAGT GTAGGCTACC  750
CTTATGGAGG AAGTGGCTTT GGTAGCTACG GAAGTGGCTA TGGCTATGGC  800
TATGGTTATG GCTATGGCTA CGGAGGCTAT ACAGACCCAA GAGCAGCAAA  850
GGGCTTCATG TTGGCCATGG CTGCCTTTTG TTTCATTGCC GCGTTGGTGA  900
TCTTTGTTAC CAGTGTTATA AGATCTGAAA TGTCCAGAAC AAGAAGATAC  950
TACTTAAGTG TGATAATAGT GAGTGCTATC CTGGGCATCA TGGTGTTTAT 1000
TGCCACAATT GTCTATATAA TGGGAGTGAA CCAACTGCT CAGTCTTCTG 1050
GATCTCTATA TGGTTACAAA ATATATGCCC TCTGCAACCA ATTTTATACA 1100
CCTGCAGCTA CTGGACTCTA CGTGGATCAG TATTTGTATC ACTACTGTGT 1150
TGTGGATCCC CAGGAGGCCA TTGCCATTGT ACTGGGGTTC ATGATTATTG 1200

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TGGCTTTTGC TTTAATAATT TTCTTTGCTG TGAAAACTCG AAGAAAGATG 1250
GACAGGTATG ACAAGTCCAA TATTTTGTGG GACAAGGAAC ACATTTATGA 1300
TGAGCAGCCC CCCAATGTCG AGGAGTGGGT TAAAAATGTG TCTGCAGGCA 1350
CACAGGACGT GCCTTCACCC CCATCTGACT ATGTGGAAAG AGTTGACAGT 1400
CCCATGGCAT ACTCTTCCAA TGGCAAAGTG AATGACAAGC GGTTTTATCC 1450
AGAGTCTTCC TATAAATCCA CGCCGGTTCC TGAAGTGGTT CAGGAGCTTC 1500
CATTAACTTC GCCTGTGGAT GACTTCAGGC AGCCTCGTTA CAGCAGCGGT 1550
GGTAACTTTG AGACACCTTC AAAAAGAGCA CCTGCAAAGG GAAGAGCAGG 1600
AAGGTCAAAG AGAACAGAGC AAGATCACTA TGAGACAGAC TACACAACTG 1650
GCGGCGAGTC CTGTGATGAG CTGGAGGAGG ACTGGATCAG GGAATATCCA 1700
CCTATCACTT CAGATCAACA AAGACAACCTG TACAAGAGGA ATTTTGACAC 1750
TGGCCTACAG GAATACAAGA GCTTACAATC AGAACTTGAT GAGATCAATA 1800
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GAAGAGTACA TGGCTGCTGC TGATGAATAC AATAGACTGA AGCAAGTGAA 1900
GGGATCTGCA GATTACAAAA GTAAGAAGAA TCATTGCAAG CAGTTAAAGA 1950
GCAAATTGTC ACACATCAAG AAGATGGTTG GAGACTATGA TAGACAGAAA 2000
ACATAGAAGG CTGATGCCAA GTTGTTTGAG AAATTAAGTA TCTGACATCT 2050
CTGCAATCTT CTCAGAAGGC AAATGACTTT GGACCATAAC CCCGGAAGCC 2100
AAACCTCTGT GAGCATCACA AAGTTTTGGG TTGCTTTAAC ATCATCAGTA 2150
TTGAAGCATT TTATAAATCG CTTTTGATAA TCAACTGGGC TGAACAACTC 2200
CAATTAAGGA TTTTATGCTT TAAACATTGG TTCTTGATATT AAGAATGAAA 2250
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2312

(3) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 522
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: polypeptide
- (v) FRAGMENT TYPE: complete sequence
- (ix) FEATURE:
 - (A) NAME/KEY: human occludin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ser	Ser	Arg	Pro	Leu	Glu	Ser	Pro	Pro	Pro	Tyr	Arg	Pro	Asp	5	10	15
Glu	Phe	Lys	Pro	Asn	His	Tyr	Ala	Pro	Ser	Asn	Asp	Ile	Tyr	Gly	20	25	30
Gly	Glu	Met	His	Val	Arg	Pro	Met	Leu	Ser	Gln	Pro	Ala	Tyr	Ser	35	40	45
Phe	Tyr	Pro	Glu	Asp	Glu	Ile	Leu	His	Phe	Tyr	Lys	Trp	Thr	Ser	50	55	60
Pro	Pro	Gly	Val	Ile	Arg	Ile	Leu	Ser	Met	Leu	Ile	Ile	Val	Met	65	70	75
Cys	Ile	Ala	Ile	Phe	Ala	Cys	Val	Ala	Ser	Thr	Leu	Ala	Trp	Asp	80	85	90
Arg	Gly	Tyr	Gly	Thr	Ser	Leu	Leu	Gly	Gly	Ser	Val	Gly	Tyr	Pro	95	100	105
Tyr	Gly	Gly	Ser	Gly	Phe	Gly	Ser	Tyr	Gly	Ser	Gly	Tyr	Gly	Tyr	110	115	120
Gly	Tyr	Gly	Tyr	Gly	Tyr	Gly	Tyr	Gly	Gly	Tyr	Thr	Asp	Pro	Arg	125	130	135
Ala	Ala	Lys	Gly	Phe	Met	Leu	Ala	Met	Ala	Ala	Phe	Cys	Phe	Ile	140	145	150
Ala	Ala	Leu	Val	Ile	Phe	Val	Thr	Ser	Val	Ile	Arg	Ser	Glu	Met	155	160	165
Ser	Arg	Thr	Arg	Arg	Tyr	Tyr	Leu	Ser	Val	Ile	Ile	Val	Ser	Ala	170	175	180
Ile	Leu	Gly	Ile	Met	Val	Phe	Ile	Ala	Thr	Ile	Val	Tyr	Ile	Met	185	190	195
Gly	Val	Asn	Pro	Thr	Ala	Gln	Ser	Ser	Gly	Ser	Leu	Tyr	Gly	Ser	200	205	210
Gln	Ile	Tyr	Ala	Leu	Cys	Asn	Gln	Phe	Tyr	Thr	Pro	Ala	Ala	Thr	215	220	225
Gly	Leu	Tyr	Val	Asp	Gln	Tyr	Leu	Tyr	His	Tyr	Cys	Val	Val	Asp	230	235	240
Pro	Gln	Glu	Ala	Ile	Ala	Ile	Val	Leu	Gly	Phe	Met	Ile	Ile	Val	245	250	255

Ala	Phe	Ala	Leu	Ile	Ile	Phe	Phe	Ala	Val	Lys	Thr	Arg	Arg	Lys
				260					265					270
Met	Asp	Arg	Tyr	Asp	Lys	Ser	Asn	Ile	Leu	Trp	Asp	Lys	Glu	His
				275					280					285
Ile	Tyr	Asp	Glu	Gln	Pro	Pro	Asn	Val	Glu	Glu	Trp	Val	Lys	Asn
				290					295					300
Val	Ser	Ala	Gly	Thr	Gln	Asp	Val	Pro	Ser	Pro	Pro	Ser	Asp	Tyr
				305					310					315
Val	Glu	Arg	Val	Asp	Ser	Pro	Met	Ala	Tyr	Ser	Ser	Asn	Gly	Lys
				320					325					330
Val	Asn	Asp	Lys	Arg	Phe	Tyr	Pro	Glu	Ser	Ser	Tyr	Lys	Ser	Thr
				335					340					345
Pro	Val	Pro	Glu	Val	Val	Gln	Glu	Leu	Pro	Leu	Thr	Ser	Pro	Val
				350					355					360
Asp	Asp	Phe	Arg	Gln	Pro	Arg	Tyr	Ser	Ser	Gly	Gly	Asn	Phe	Glu
				365					370					375
Thr	Pro	Ser	Lys	Arg	Ala	Pro	Ala	Lys	Gly	Arg	Ala	Gly	Arg	Ser
				380					385					390
Lys	Arg	Thr	Glu	Gln	Asp	His	Tyr	Glu	Thr	Asp	Tyr	Thr	Thr	Gly
				395					400					405
Gly	Glu	Ser	Cys	Asp	Glu	Leu	Glu	Glu	Asp	Trp	Ile	Arg	Glu	Tyr
				410					415					420
Pro	Pro	Ile	Thr	Ser	Asp	Gln	Gln	Arg	Gln	Leu	Tyr	Lys	Arg	Asn
				425					430					435
Phe	Asp	Thr	Gly	Leu	Gln	Glu	Tyr	Lys	Ser	Leu	Gln	Ser	Glu	Leu
				440					445					450
Asp	Glu	Ile	Asn	Lys	Glu	Leu	Ser	Arg	Leu	Asp	Lys	Glu	Leu	Asp
				455					460					465
Asp	Tyr	Arg	Glu	Glu	Ser	Glu	Glu	Tyr	Met	Ala	Ala	Ala	Asp	Glu
				470					475					480
Tyr	Asn	Arg	Leu	Lys	Gln	Val	Lys	Gly	Ser	Ala	Asp	Tyr	Lys	Ser
				485					490					495
Lys	Lys	Asn	His	Cys	Lys	Gln	Leu	Lys	Ser	Lys	Leu	Ser	His	Ile
				500					505					510
Lys	Lys	Met	Val	Gly	Asp	Tyr	Asp	Arg	Gln	Lys	Thr			
				515					520					

(4) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: peptide
- (v) FRAGMENT TYPE: synthetic peptide
- (ix) FEATURE:
 - (D) OTHER INFORMATION: construct used in experiments
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Cys Asp Arg Gly Tyr Gly Thr Ser Leu Leu Gly Gly Ser Val Gly
5 10 15

Tyr Pro Tyr Gly Gly Ser Gly Phe Gly
20

(5) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: peptide
- (v) FRAGMENT TYPE: synthetic peptide
- (ix) FEATURE:
 - (D) OTHER INFORMATION: construct used in experiments
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Cys Ser Tyr Gly Ser Gly Tyr Gly Tyr Gly Tyr Gly Tyr Gly Tyr
5 10 15

7/7
 Gly Tyr Gly Gly Tyr Thr Asp Pro Arg
 20

(6) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: peptide

(v) FRAGMENT TYPE: synthetic peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: construct used in experiments

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Asn	His	Tyr	Ala	Pro	Ser	Asn	Asp	Ile	Tyr	Gly	Gly	Glu	Met	Val
				5					10					15
His	Arg	Pro	Met	Leu										
				20										

(7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: peptide

(v) FRAGMENT TYPE: synthetic peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: construct used in experiments

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ala	Ser	Gln	Gln	Val	Tyr	Arg	Lys	Asp	Pro	Cys
				5					10	